

PATENT

Attorney Docket No.

DX0804K

CN 028008

RECEIVED

JUL 3 1 2001

TECH CENTER 1600/2900

Art Unit: 1647

COMPUTER READABLE SEQUENCE
SUBMISSION

20/c
H.G.J
8/1/01

Palo Alto, California 94304
July 17, 2001

Sir:

**COMPLIANCE WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

In reply to receipt of a "Notice to Comply" with requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures dated May 3, 2001, (paper no.18), for the above-identified application, in accordance with 37 CFR § 1.821 - 1.825, Applicants hereby submit: (1) a write-protected diskette containing a computer-readable submission for the "Sequence Listing"; and (2) a "Sequence Listing" paper copy of the contents of the diskette.

REMARKS

Enclosed is a write protected floppy diskette with the sequence listing generated by the Patent Office's PATENTIN 3.1 program. The Diskette should comply with the requirements of 37 CFR §1.824 and is IBM PC compatible with a PC-DOS/MS-DOS operating system. If the diskette has been damaged, please call Applicants and a replacement diskette will be provided. A hard paper copy printout of the diskette is attached thereto.

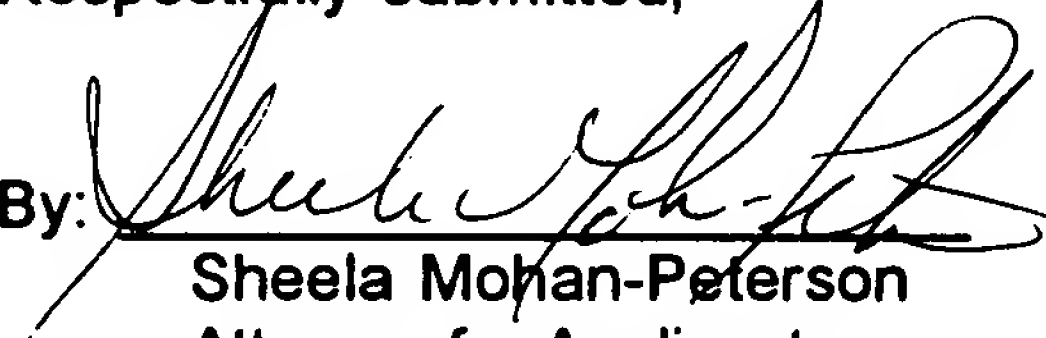
I hereby state the informational contents of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are believed to be the same. This submission introduces no new matter, since enclosed sequences are the same as sequences which were submitted in priority documents.

Applicants have invested over ten hours of significant labor and care in preparing the present submission. The enclosed items are a bona fide effort to bring the present application into full compliance with the rules for sequence submissions. Should this not be the case, Applicants respectfully request notification of specific deficiencies and an opportunity for remedy, as described in 37 CFR 1.135(c).

Applicants believe that no fees are required; however, if any fees are required by the present Response, the Commissioner is authorized to charge any fees or credit any overpayment to DNAX Research Institute Deposit Account No. 04-1239.

Date: July 17, 2001

Respectfully submitted,

By: 
Sheela Mohan-Peterson
Attorney for Applicants
Reg. No. 41,201

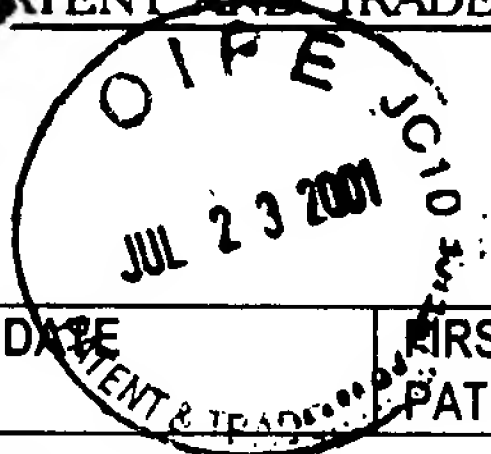
enclosures and attachments:
request for an extension of time
one write-protected diskette (CRM)
paper copy of contents of diskette
copy of notice to comply

DNAX Research Institute
901 California Avenue
Palo Alto, California 94304-1104
Main: (650) 852-9196
Direct: (650) 496-1244
Fax: (650) 496-1200



UNITED STATES PATENT AND TRADEMARK OFFICE

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UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, DC 20231
www.uspto.gov



APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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09/265,540

3-8-99

Parham

DXO 804K

EXAMINER

S. Wegert

ART UNIT

PAPER

1647

18

DATE MAILED:

5-8-01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

The communication filed 3/27/01 is not fully responsive to the Office communication mailed 3/07/01 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid ABANDONMENT of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner Sandra Wegert, Art Unit 1647, whose telephone number is (703) 308-9346

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

Elizabeth C. Hummer

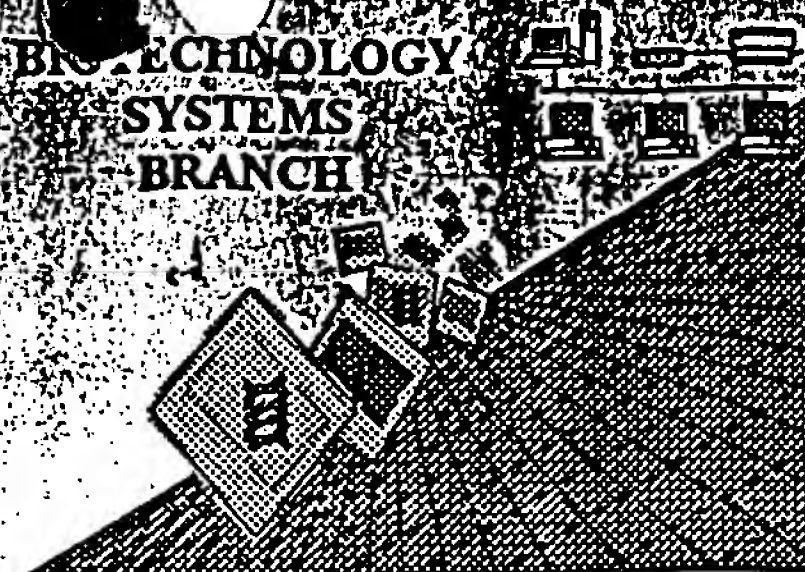
ELIZABETH HUMMER
PRIMARY EXAMINER

Available Copy

RAW SEQUENCE LISTING
ERROR REPORT

4/9/01

BIO TECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540P

Source: 1647

Date Processed by STIC: 3/27/2001

RECEIVED

APR 04 2001

TECH CENTER 1600/29

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

703-308
4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/265,540

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS"
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
"file," resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1647

RAW SEQUENCE LISTING

DATE: 03/27/2001

PATENT APPLICATION: US/09/265,540D

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

Does Not Comply
Corrected Diskette Needed

see pp. 2-3, 5

3 <110> APPLICANT: Parham, Christi L.
 4 Moore, Kevin W.
 5 Murgolo, Nicholas J.
 6 Bazan, J. Fernando
 8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 10 <130> FILE REFERENCE: DX0804K
 12 <140> CURRENT APPLICATION NUMBER: 09/265,540D
 13 <141> CURRENT FILING DATE: 1999-03-08
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
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 22 <213> ORGANISM: primate
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (132)..(1064)
 28 <220> FEATURE:
 29 <221> NAME/KEY: unsure
 30 <222> LOCATION: (567)
 31 <223> OTHER INFORMATION: n at position 567; n may be A, C, G, or T;
 32 translated amino acid depends on genetic code
 34 <220> FEATURE:
 35 <221> NAME/KEY: unsure
 36 <222> LOCATION: (573)
 37 <223> OTHER INFORMATION: n at position 573; n may be A, C, G, or T;
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 41 <221> NAME/KEY: unsure
 42 <222> LOCATION: (1336)
 43 <223> OTHER INFORMATION: n at position 1336; n may be A, C, G, or T;
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 48 <222> LOCATION: (1342)
 49 <223> OTHER INFORMATION: n at position 1342; n may be A, C, G, or T;
 50 translated amino acid depends on genetic code
 52 <220> FEATURE:
 53 <221> NAME/KEY: unsure
 54 <222> LOCATION: (1369)
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 61 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120
 63 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
 64 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001
TIME: 10:50:04

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Output Set: N:\CRF3\03272001\I265540D.raw

65	1	5	10	
67	agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca	218		
68	Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr			
69	15 20 25			
71	gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca	266		
72	Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser			
73	30 35 40 45			
75	acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga	314		
76	Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly			
77	50 55 60			
79	gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg	362		
80	Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu			
81	65 70 75			
83	tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa	410		
84	Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu			
85	80 85 90			
87	ggg cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac	458		
88	Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr			
89	95 100 105			
91	aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc	506		
92	Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser			
93	110 115 120 125			
95	atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct	554		
96	Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro			
97	130 135 140			
W--> 99	ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag	602		
W--> 100	Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu			
101	145 150 155			
103	gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag	650		
W--> 104	Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu			
105	160 165 170			
107	cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca	698		
108	Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro			
109	175 180 185			
111	gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc	746		
112	Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala			
113	190 195 200 205			
115	cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca	794		
W--> 116	Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr			
117	210 215 220			
119	gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg	842		
W--> 120	Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu			
121	225 230 235			
123	ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc	890		
124	Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe			
125	240 245 250			
127	gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg	938		
128	Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val			
129	255 260 265			

*move amino acids directly
under respective
codon*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001
TIME: 10:50:04

Input Set : A:\804k.app
Output Set: N:\CRF3\03272001\I265540D.raw

131 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986
132 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
133 270 275 280 285
135 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
136 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
137 290 295 300
139 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084
140 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
141 305 310
143 ggtgaagccg agaacctggt ctgcatgaca tggaaacccat gagggggacaa gttgtgtttc 1144
145 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgct tacaagtcta 1204
147 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
149 gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324
151 cttcateccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg 1381
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156 <212> TYPE: PRT
157 <213> ORGANISM: primate
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161 1 5 10 15
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164 20 25 30
166 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
167 35 40 45
169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
170 50 55 60
172 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
173 65 70 75 80
175 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
176 85 90 95
178 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
179 100 105 110
181 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
182 115 120 125
184 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
185 130 135 140
W--> 187 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
188 145 150 155
W--> 190 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
191 165 170 175
193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
194 180 185 190
196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
197 195 200 205
W--> 199 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
200 210 215 220
W--> 202 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
203 225 230 235 240

*all item 10 on
Even Summary
Sheet*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

205 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 206 245 250 255
 208 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 209 260 265 270
 211 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 212 275 280 285
 214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 215 290 295 300
 217 Leu Leu Arg Ala Trp Ile Ser
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 237 1 5 10 15
 239 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
 240 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 241 20 25 30
 243 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
 244 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 245 35 40 45
 247 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
 248 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
 249 50 55 60
 251 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
 252 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 253 65 70 75 80
 255 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
 256 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
 257 85 90 95
 259 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
 260 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
 261 100 105 110
 263 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
 264 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
 265 115 120 125
 267 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433
 268 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
 269 130 135 140
 271 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

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275 ctg gtg aaa tac tgg ttt cac tct ccg cca' agc atc cca tca caa atc 529
276 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
277          165          170          175
279 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577
280 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
281          180          185          190
283 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625
284 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
285          195          200          205
287 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673
288 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
289          210          215          220
291 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggt ctgagccgag 724
292 Gln Asn Ser Gly Ala Val Cys
293 225          230
295 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc 784
297 aaaaggccccg tcagtgcctg tgaagatgta acgggtctca tgggggagac aagcttattg 844
299 atttttttct tcaaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904
301 tatgtccccg aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgta 964
303 gcaaatgggc gtctggcacg cctctgacac ttttctgtca gcagccagga cagaggtcc 1024
305 cctccttgat gaagcccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084
307 gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144
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316 <212> TYPE: PRT
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326 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
327 35 40 45
W--> 329 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His (Xaa) see item 10
330 50 55 60
332 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
333 65 70 75 80
335 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
336 85 90 95
338 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
339 100 105 110
341 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
342 115 120 125
344 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
345 130 135 140

```

VERIFICATION SUMMARY
 PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001
 TIME: 10:50:05

Input Set : A:\804k.app
 Output Set: N:\CRF3\03272001\I265540D.raw

L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
 L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
 L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
 L:187 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
 L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
 L:190 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
 L:190 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
 L:190 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
 L:190 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
 M:340 Repeated in SeqNo=2
 L:199 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
 L:199 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
 L:199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
 L:199 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
 L:202 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
 L:202 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
 L:202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
 L:202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
 L:248 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
 L:248 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
 L:329 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
 L:329 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
 L:329 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
 L:329 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
 L:329 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4